

Structure of the PCA3 transcription unit



APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

[illegible]

379 531

1	99	264	447	986	2037
1	98	263	446	985	

11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1041 1042 1043 1044 10

>---PCA3--->

>-EXON1->-----EXON2----->-----EXON3-----EXON4a-----EXON4b----->
 1 |-----EXON2-----EXON3-----EXON4a-----EXON4b----->
 1 |-----EXON2-----EXON3-----EXON4a-----EXON4b----->

711-2A

1) EXON1, 2) EXON2, 3) EXON3, 4) EXON4A, 5) EXON4b, PCA3 (amino acids)
(poly-A-addition signals are underlined)

CON) : Range= 1 to 2037

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Name Base

1 1 agaagctggc atcagaaaaa cagagggggag atttgtgtgg ctgcagccga gggagaccag

CON 1 AGAAGCTGGC ATCAGAAAAA CAGAGGGGAG ATTTGTGTGG CTGCAGCCGA GGGAGACCAG

1 1 gaagatctgc atggtggga ggacctgatg atacagag
61

ga attacaacac atatacttag

File # 2B

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

CON 300 AGGCCACACA TCTGCTGAAA TGGAGATAAT TAACATCACT AGAAACAGCA AGATGACAAAT

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[illegible]

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

3 97 ataatgtcta agtagtgac atgttttttg cacatttcc agcccccttt aaatatcca cacaca

CON 360 ATAATGTCTA AGTAGTGAC ATGTTTTTG CACATTTC AGCCCCCTTT AAATATCCA CACACA

PCA3 1 M F L H I S S P F K Y P H T

3 158 caggaagca caaaaggaa gcacagag

4 1 a tccctggga gaaatgccc ggccgccat cttggg

CON 421 CAGGAAGCA CAAAGGAA GCACAGAGA TCCCTGGGA GAAATGCCC GGCCGCCAT CTGGG

PCA3 15 Q E A Q K E A Q R S L G E M P G R H L G

4 35 tcatcgatg agcctcgcc ctgtgcctg gtcccgcctt gtgAGGGAA GGACATTAG AAA

CON 481 TCATCGATG AGCCTCGCC CTGTGCCTG GTCCCGCTT GTGAGGGAA GGACATTAG AAA

PCA3 35 S S M S L A L C L V P L V R E G H ***

4 93 ATGAAATTGAT GTGTTCCCTTA AAGGATGGC AGGAAAACAG ATCCTGTTGT GGATATTAT

CON 538 ATGAAATTGAT GTGTTCCCTTA AAGGATGGC AGGAAAACAG ATCCTGTTGT GGATATTAT

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APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

00EFS0"ET20460

4 153 TTGAACGGGA TTACAGATT TAAATGAAGT CACAAAGTGA GCATTACCA TGAGAGGAAA

CON 598 TTGAACGGGA TTACAGATT TAAATGAAGT CACAAAGTGA GCATTACCA TGAGAGGAAA

4 213 ACAGACGAGA AAATCTTGAT GGCTTCACAA GACATGCAAC AAACAAAATG GAATACTGTG

CON 658 ACAGACGAGA AAATCTTGAT GGCTTCACAA GACATGCAAC AAACAAAATG GAATACTGTG

4 273 ATGACATGAG GCAGCCAAGC TGGGGaggag ataaccacgg ggcaGAGGGT CAGGATTCTG

CON 718 ATGACATGAG GCAGCCAAGC TGGGGAGGAG ATAACCACGG GGCAGAGGGT CAGGATTCTG

4 333 GCCCTGCTGC CTAAACTGTG CGTTCATAAC CAAATCATTT CATATTTCTA ACCCTCAAAA

CON 778 GCCCTGCTGC CTAAACTGTG CGTTCATAAC CAAATCATTT CATATTTCTA ACCCTCAAAA

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DEF 90" EF 20460

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

4 393 CAAAGCTGTT GTAATATCTG ATCTCTACGG TTCCTTCTGG GCCCAACATT CTCCATATAT

CON 838 CAAAGCTGTT GTAATATCTG ATCTCTACGG TTCCTTCTGG GCCCAACATT CTCCATATAT

4 453 CCAGCCACAC TCATTTTAA TATTAGTTC CCAGATCTGT ACTGTGACCT TTCTACACTG

CON 898 CCAGCCACAC TCATTTTAA TATTAGTTC CCAGATCTGT ACTGTGACCT TTCTACACTG

4 513 TAGAATAACA TTAATCATTT TGTTCAA 6/17

5 1

GA CCCTTCGTGT TGCTGCCCTAA TATGTAGCTG

CON 958 TAGAATAACA TTAATCATTT TGTTCAAAGA CCCTTCGTGT TGCTGCCCTAA TATGTAGCTG

5 33 ACTGTTTTTC CTAAGGAGTG TTCTGGCCCA GGGATCTGT GAACAGGCTG GGAAGCATCT

CON 1018 ACTGTTTTTC CTAAGGAGTG TTCTGGCCCA GGGATCTGT GAACAGGCTG GGAAGCATCT

5 93 CAAGATCTTT CCAGGGTTAT ACTTACTAGC ACACAGCATG ATCATTACGG AGTGAATTAT

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APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
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CON 1078	CAAGATCTTT	CCAGGGTTAT	ACTTACTAGC	ACACAGCATG	ATCATTACGG	AGTGAATTAT
5	CTAATCAACA	TCATCCTCAG	TGTCTTTGCC	CATACTGAAA	TTCATTTCCC	ACTTTGTGTC
CON 1138	CTAATCAACA	TCATCCTCAG	TGTCTTTGCC	CATACTGAAA	TTCATTTCCC	ACTTTGTGTC
5	CCATTCTCAA	GACCTCAAAA	TGTCATTCCA	TTAATATCAC	AGGATTAACT	TTTTTTTTTTA
CON 1198	CCATTCTCAA	GACCTCAAAA	TGTCATTCCA	TTAATATCAC	AGGATTAACT	TTTTTTTTTTA
5	ACCTGGAAGA	ATTCAATGTT	ACATGCAGCT	ATGGGAATTT	AATTACATAT	TTTGTGTTTTCC
CON 1258	ACCTGGAAGA	ATTCAATGTT	ACATGCAGCT	ATGGGAATTT	AATTACATAT	TTTGTGTTTTCC
5	AGTGCAAAGA	TGACTAAGTC	CTTTATCCCT	CCCCTTTGTT	TGATTTTTTTT	TCCAGTATAAA
CON 1318	AGTGCAAAGA	TGACTAAGTC	CTTTATCCCT	CCCCTTTGTT	TGATTTTTTTT	TCCAGTATAAA

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APPROVED	O.G.FIG.	
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SEQUENCE

5 393 AGTTAAATG CTTAGCCTTG TACTGAGGCT GTATACAGCA CAGCCTCTCC CCATCCCCTCC
 CON 1378 AGTTAAATG CTTAGCCTTG TACTGAGGCT GTATACAGCA CAGCCTCTCC CCATCCCCTCC

 5 453 AGCCTTATCT GTCATCACCA TCAACCCCTC CCATNYSACC TAAACAAAAT CTAACCTGTA
 CON 1438 AGCCTTATCT GTCATCACCA TCAACCCCTC CCATNYSACC TAAACAAAAT CTAACCTGTA

 5 513 ATTCCCTTGAA CATGTCAGGN CATACTTTC TCCTTCTGCC TGAGAAGCTC TTCCTTGTCT
 CON 1498 ATTCCCTTGAA CATGTCAGGN CATACTTTC TCCTTCTGCC TGAGAAGCTC TTCCTTGTCT

 5 573 CTTAANTCTA GAATGATGTA AAGTTTGTAA TAAGTTGACT ATCTTACTTC ATGCAAAGAA
 CON 1558 CTTAANTCTA GAATGATGTA AAGTTTGTAA TAAGTTGACT ATCTTACTTC ATGCAAAGAA

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APPROVED	O.G. FIG.	
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DRAFTSHAH		

00ET50" ET 220460

5 633 GGGACACATA TGAGATTTCAT CATCACATGA GACAGCAAAT ACTAAAAGTG TAATTGATT
CON 1618 GGGACACATA TGAGATTTCAT CATCACATGA GACAGCAAAT ACTAAAAGTG TAATTGATT

5 693 ATAAGAGTTT AGATAAATAT ATGAAATGCA AGAKCCACAG AGGGAATGTT TATGGGGCAC
CON 1678 ATAAGAGTTT AGATAAATAT ATGAAATGCA AGAKCCACAG AGGGAATGTT TATGGGGCAC

5 753 GTTTGTAGC CTGGGATGTG AAGMAAAGGC AGGGAACCTC ATAGTATCTT ATATAATATA
CON 1738 GTTTGTAGC CTGGGATGTG AAGMAAAGGC AGGGAACCTC ATAGTATCTT ATATAATATA

5 813 CTTTCATTCT CTATCTCTAT CACAATATCC AACAAAGCTTT TCACAGAATT CATGCAGTGC
CON 1798 CTTTCATTCT CTATCTCTAT CACAATATCC AACAAAGCTTT TCACAGAATT CATGCAGTGC

5 873 AAATCCCCAA AGGTAACCTT TATCCATTTC ATGGTGAGTG CGCTTTAGAA TTTTGGCAAA

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006790" ET 20460

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

WO 98/45420

09/402713

PCT/CA98/00346

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CON 1858 AAATCCCCAA AGGTAACCTT TATCCATTTC ATGGTGAGTG CGCTTTAGAA TTTTGGCAAA

5 933 TCATACTGGT CACTTATCTC AACTTTGAGA TGTGTTTGTC CTTGTAGTTA ATTGAAAGAA

CON 1918 TCATACTGGT CACTTATCTC AACTTTGAGA TGTGTTTGTC CTTGTAGTTA ATTGAAAGAA

5 993 ATAGGGCACT CTTgtgagcc actttagggt tcaactcctgg caataaagaa tttacaaga

CON 1978 ATAGGGCACT CTTgtgagcc actttagggt tcaactcctgg caataaagaa tttacaaga

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APPROVED BY DRAFTSMAN	O.G. FIG.	
	CLASS	SUBCLASS

PCA3 cDNA clones

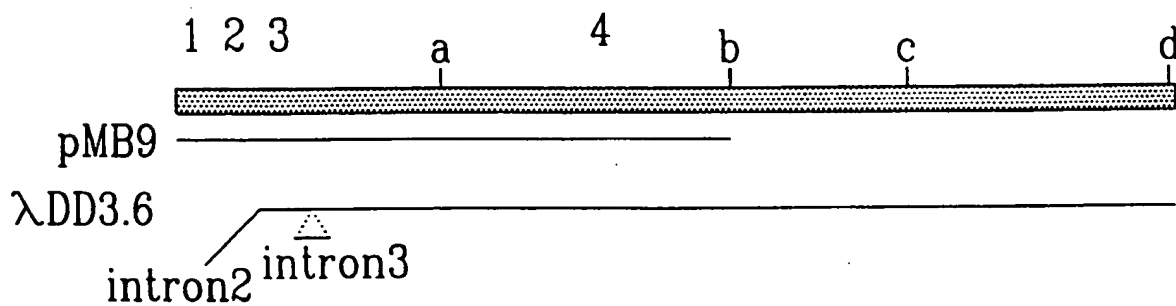
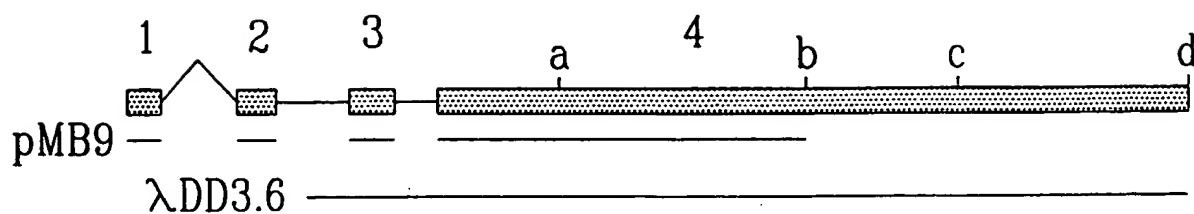


FIG. 3

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APPROVED	O.G. FIG.
BY	CLASS SUBCLASS
DRAFTSHAH	

PE | S1 | 5' RACE | 5' RACE | CDNAS
▼ ▼ ▼ ▼ ▼
...g ACAGAAG AAATAGCAAG TGCCGAGAAG CTGGCATCAG
L → TSS L → pMB9
AAAAACAGAG GGGAGATTG TGTGGCTGCA GCCGAGGGAG ACCAGGAAGA
TCTGCATGGT GGGAAGGACC TGATGATACA GAG gt ...
splice site

FIG. 4

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

Sequence PCA3 cDNA and PCA3 protein:

1 ACAGAAGAAA TAGCAAGTGC CGAGAAGCTG GCATCAGAAA AACAGAGGGG AGATTGTGT
61 GGCTGCAGCC GAGGGAGACC AGGAAGATCT GCATGGTGGG AAGGACCTGA TGATACAGAG
121 GAATTACAAC ACATATACTT AGTGTTTCAA TGAACACCAA GATAAATAAG TGAAGAGCTA
181 GTCCGCTGTG AGTCTCCTCA GTGACACAGG GCTGGATCAC CATCGACGGC ACTTTCTGAG
241 TACTCAGTGC AGCAAAGAAA GACTACAGAC ATCTCAATGG CAGGGGTGAG AAATAAGAAA
301 GGCTGCTGAC TTTACCATCT GAGGCCACAC ATCTGCTGAA ATGGAGATAA TTAACATCAC

APPROVED	O.G.FIG.	
BY	CLASS	SUBCLASS
DRAFTSHAH		

"DETENTION" 20040405

361 TAGAAACAGC AAGATGACAA TATAATGTCT AAGTAGTGAC **ATG**TTTTTTC ACATTTCACAG
PCA3 1 M F L H I S S

421 CCCCTTTAAA TATCCACACA CACAGGAAGC ACAAAGGAA GCACAGAGAT CCCTGGGAGA
PCA3 8 P F K Y P H T Q E A Q K E A Q R S L G E

481 AATGCCCGGC CGCCATCTTG GGTCAATCGAT GAGCCTCGCC CTGTGCCCTGG TCCCGCTTGT
PCA3 28 M P G R H L G S S M S L A L C L V P L V

541 GAGGGAAGGA CATTAGAAA TGAATTGATG TGTTCCCTTAA AGGATGGGCA GGAAACACAGA
PCA3 48 R E G H *

601 TCCTGTTGTG GATATTATT TGAACGGGAT TACAGATTG AAATGAAGTC ACAAAGTGAG

661 CATTACCAAT GAGAGGAAA CAGACGAGAA AATCTTGATG GCTTCACAAG ACATGCAACA

721 AACAAAATGG AATACTGTGA TGACATGAGG CAGCCAAGCT GGGGAGGAGA TAACCACGGG

781 GCAGAGGGTC AGGATTCTGG CCTGCTGCC TAAACTGTGC GTTCATAACC AAATCATTTT

841 ATATTCTTAA CCTCAAAAC AAAGCTGTTG TAATATCTGA TCTCTACGGT TCCTTCTGGG

901 CCCAACATTC TCCATATATC CAGCCACACT CATTTTAAAT ATTAGTTCC CAGATCTGTA

961 CTGTGACCCTT TCTACACTGT AGAATAACAT TACTCATTTT GTTCAAAGAC CCTTCGTGTT

1021 GCTGCCTAAT ATGTAGCTGA CTGTTTTTCC TAAGGAGTGT TCTGGCCCAG GGGATCTGTG

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APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

DELETED" ET 20460

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1081 AACAGGCTGG GAAGCATCTC AAGATCTTTC CAGGGTTATA CTTACTAGCA CACAGCATGA
 1141 TCATTACGGA GTGAATTATC TAATCAACAT CATCCTCAGT GTCTTTGCC ATACTGAAAT
 1201 TCATTTCCCA CTTTGTGCC CATTCTCAAG ACCTCAAAAT GTCATTCCAT TAATATCACA
 1261 GGATTAACTT TTTTTTTTAA CCTGGAAGAA TTCAATGTTA CATGCAGCTA TGGGAATTTA
 1321 ATTACATATT TTGTTTTTCCA GTGCAAAAGAT GACTAAGTCC TTTATCCCTC CCCTTTGTTT
 1381 GATTTTTTTT CCAGTATAAA GTTAAATGC TTAGCCTTGT ACTGAGGCTG TATACAGCAC
 1441 AGCCTCTCCC CATCCCTCCA GCCTTATCTG TCATCACCAT CAACCCCTCC CATAACACCT
 1501 AAACAAAATC TAACTTGTA TCCCTTGAAC ATGTCAGGAC ATACATTATT CCTTCTGCCT
 1561 GAGAAAGCTCT TCCTTGCTC TTAAATCTAG AATGATGTAA AGTTTTGAAT AAGTTGACTA
 1621 TCTTACTTCA TGCAAAGAAG GGACACATAT GAGATTTCATC ATCACATGAG ACAGCAAATA
 1681 CTAAAAGTGT AATTTGATTA TAAGAGTTTA GATAAATATA TGAAATGCAA GAGCCACAGA
 1741 GGAATGTTT ATGGGGCACG TTTGTAAGCC TGGGATGTGA AGCAAAGGCA GGAACCTCA
 1801 TAGTATCTTA TATAATATAC TTCATTTTCTC TATCTCTATC ACAATATCCA ACAAGCTTTT
 1861 CACAGAATTC ATGCAGTGCA AATCCCCAAA GGTAACCTTT ATCCATTTC TGGTGAGTGC

FIG. 50

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
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1921 GCTTTAGAAAT TTTGGCAAAT CATACTGGTC ACTTATCTCA ACTTTGAGAT GTGTTTGTCC
1981 TTGTAGTTAA TTGAAAGAAA TAGGGCACTC TTGTGAGCCA CTTTAGGGTT CACTCCCTGGC
2041 AATAAAGAAT TTACAAAGAG CTACTCAGGA CCAGTTGTTA AGAGCTCTGT GTGTGTGTGT
2101 GTGTGTGTGT GAGGTACAT GCCAAAGTGT GCCTCTCTCT CTTGACCCAT TATTTACAGAC
2161 TTAAACAAG CATGTTTCA AATGGCACTA TGAGCTGCCA ATGATGTATC ACCACCATAT
2221 CTCATTATTC TCCAGTAAAT GTGATAATAA TGTCATCTGT TAACATAAAA AAAGTTTGAC
2281 TTCACAAAAG CAGCTGGAAA TGGACAACCA CAATATGCAT AAATCTAACT CCTACCATCA
2341 GCTACACACT GCTTGACATA TATTGTTAGA AGCACCTCGC ATTTGTGGGT TCTCTTAAGC
2401 AAAATACTTG CATTAGGTCT CAGCTGGGGC TGTGCATCAG GCGGTTTGAG AAATATTCAA
2461 TTCTCAGCAG AAGCCAGAAT TTGAATTCCC TCATCTTTTA GGAATCATTT ACCAGGTTTG
2521 GAGAGGATTC AGACAGCTCA GGTGCTTTCA CTAATGTCTC TGAACCTCTG TCCCTCTTTG
2581 TGTTCATGGA TAGTCCAATA AATAATGTTA TCTTTGAACT GATGCTCATA GGAGAGAATA
2641 TAAGAACTCT GAGTGATATC AACATTAGGG ATTCAAAGAA ATATTAGATT TAAGCTCACA
2701 CTGGTCAAAA GGAACCAAGA TACAAAGAAC TCTGAGCTGT CATCGTCCCC ATCTCTGTGA

FIG. 5E

APPROVED	O.G. FIG.	
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SEQUENCE "E" 20450

2761 GCCACAACCA ACAGCAGGAC CCAACGCATG TCTGAGATCC TTAAATCAAG GAAACCAGTG
 2821 TCATGAGTTG AATTCTCCTA TTATGGATGC TAGCTTCTGG CCATCTCTGG CTCTCCTCTT
 2881 GACACATATT AGCTTCTAGC CTTTGCTTCC ACGACTTTTA TCTTTTCTCC AACACATCGC
 2941 TTACCAATCC TCTCTCTGCT CTGTGCTTT GGACTTCCCC ACAAGAATT CAACGACTCT
 3001 CAAGTCCTTT CTTCATCCC CACCATAAC CTGAATTGCC TAGACCCTTA TTTTATTAA
 3061 TTTCCAATAG ATGCTGCCCTA TGGGCTAATA TTGCTTTAGA TGAACATTAG ATATTTAAAG
 3121 TCTAAGAGGT TCAAAATCCA ACTCATTATC TTCTCTTTCT TTCACCTCCC CTGCTCCTCT
 3181 CCTATATTA CTGATTGACT GAACAGGATG GTCCCCAAGA TGCCAGTCAA ATGAGAAACC
 3241 CAGTGGCTCC TTGTGGATCA TGCATGCAAG ACTGCTGAAG CCAGAGGATG ACTGATTACG
 3301 CCTCATGGT GGAGGGGACC ACTCCTGGGC CTTCTGTGATT GTCAGGAGCA AGACCTGAGA
 3361 TGCTCCCTGC CTTCAGTGTC CTCTGCATCT CCCCTTTCTA ATGAAGATCC ATAGAATTG
 3421 CTACATTGA GAATCCAAT TAGGAACTCA CATGTTTTAT CTGCCCTATC AATTTTTTAA
 3481 ACTTGCTGAA AATTAAGTTT TTTCAAATC TGTCCTTGTA AATTACTTT TCTTACAGTG
 3541 TCTTGGCATA CTATATCAAC TTTGATTCTT TGTACAAC TT

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